Table 1S: Description of selected SNPs

Gene Name	Chromosome	SNP Name	chromosome position (GRCh38p10)	Most severe consequence	HGVS Name	Reference sequence	MAF	tag SNP
COX5A	15	rs1133322	74920016	DOWNSTREAM	c.*436T>C	NM_004255.3	0.25 (G)	1**
COX5B	2	rs1470625	97649028	DOWNSTREAM	g.97649028C>A	NC_000012.12	0.46 (C)	2**
		rs17022045	97645225	UPSTREAM	c.-862C>G	NM_001862.2	0.13 (G)	1**
COX6A1	12	rs17431357	120442631	UPSTREAM	g.120442631C>T	NC_000012.12	0.04 (T)	
		rs12310837	120442769	UPSTREAM	g.120442769A>G	NC_000012.12	0.15 (G)	
		rs2076022	120437987	UPSTREAM	c.-140C>T	NM_004373.3	0.49 (T)	2**
COX6B1	19	rs4806187	35658859	DOWNSTREAM	c.*212A>G	NM_001863.4	0.33 (A)	1**
COX6C	8	rs1130569	99887565	SYNONYMOUS_CODING	p.Tyr56=	NP_004365.1	0.25 (A)	
		rs4626565	99878314	INTRONIC	c.*16-49A>G	NM_004374.3	0.23 (C)	1**
COX7A1	19	rs753420	36152793	5PRIME_UTR	c.-386A>C	NM_001864.3	0.40 (G)	1**
		rs7255180	36149417	INTRONIC	c.722-161C>T	NM_001003962.2	0.02 (T)	
COX7A2	6	rs436898	75235832	DOWNSTREAM	g.75235832A>C	NC_000006.12	0.16 (A)	
		rs683943	75252092	UPSTREAM	g.75252092C>G	NC_000006.13	0.05 (C)	
		rs9360898	75243989	5PRIME_UTR	c.-159A>C	NM_001865.3	0.21 (G)	3**
COX7B2	4	rs9790574	46732884	DOWNSTREAM	g.46732884C>T	NC_000004.12	0.25 (T)	
COX7C	5	rs16902285	86621753	DOWNSTREAM	g.86621753T>G	NC_000005.10	0.07 (G)	
		rs13161296	86617233	UPSTREAM	c.-823C>T	NM_001867.2	0.01 (T)	1**
		rs2410718	86622655	DOWNSTREAM	g.86622655G>A	NC_000005.10	0.12 (A)	
COX8C	14	rs2089095	93350593	INTRONIC	c.-351+17070C>G	NM_020818.4	0.11 (G)	
NDUFS1	2	rs1053517	206122291	DOWNSTREAM	g.206122291A>G	NC_000002.12	0.49 (G)	1**
		rs3770989	206124027	3PRIME_UTR	c.*158T>C	NM_001199981.1	0.03 (G)	3**
		rs11548670	206147759	SYNONYMOUS_CODING	p.Asp102=	NP_001186910.1	0.07 (G)	2**

Table 1S cont: Description of selected SNPs

Gene Name	Chromosome	SNP Name	chromosome position (GRCh38p10)	Most severe consequence	HGVS Name	Reference sequence	MAF	tag SNP
NDUFS2	1	rs4656994	161210087	INTRONIC	c.703-24G>A	NM_001166159.1	0.26 (A)	3**
		rs1136224	161214307	3PRIME_UTR	c.*366A>G	NM_001166159.1	0.18 (G)	6**
		rs1136207	161213726	SYNONYMOUS_CODING	p.Ala430=	NP_001159631.1	0.16 (T)	
		rs4656993	161206347	INTRONIC	c.203-60A>G	NM_001166159.1	0.30 (A)	
		rs11587213	161215085	UPSTREAM	g.161215085A>G	NC_000001.11	0.15 (G)	5**
NDUFS3	11	rs10742816	47585432	UPSTREAM	g.47585432C>T	NC_000011.10	0.25 (C)	1**
NDUFS4	5	rs31304	53646253	SYNONYMOUS_CODING	p.Gly66=	NP_001304980.1	0.06 (A)	
		rs567	53683267	3PRIME_UTR	c.*46G>A	NM_002495.3	0.38 (A)	3**,5**,6**
		rs535277	53658684	INTRONIC	c.424+60T>G	NM_002495.3	0.29 (G)	
NDUFS5	1	rs1984600	39026255	UPSTREAM	c.-150G>C	NM_004552.2	0.46 (G)	1**
		rs11205591	39035577	DOWNSTREAM	g.39035577C>G	NC_000001.11	0.24 (G)	2**
NDUFS6	5	rs11953620	1818516	DOWNSTREAM	g.1818516C>T	NC_000005.10	0.42 (T)	
		rs4975851	1817222	DOWNSTREAM	g.1817222C>T	NC_000005.10	0.38 (C)	
NDUFS7	19	rs11666067	1389518	non coding transcript exon variant	c.228+580C>A	NM_024407.4	0.46 (A)	
SDHB	1	rs1022580	17033181	INTRONIC	c.201-36G>T	NM_003000.2	0.04 (C)	1**
		rs2647169	17044728	INTRONIC	c.200+33G>A	NM_003000.2	0.11 (T)	3**
		rs11203280	17016288	UPSTREAM	g.17016288G>T	NC_000001.11	0.50 (G)	
		rs9435739	17016429	UPSTREAM	g.17016429G>A	NC_000001.11	0.48 (A)	

Table 1S cont2: Description of selected SNPs

Gene Name	Chromosome	SNP Name	chromosome position (GRCh38p10)	Most severe consequence	HGVS Name	Reference sequence	MAF	tag SNP
SDHC	1	rs4600063	161363401	3PRIME_UTR	g.161363401A>G	NC_000001.11	0.17 (G)	
		rs13374037	161365491	3PRIME_UTR	g.161365491T>A	NC_000001.11	0.17 (A)	3**
SDHD	11	rs10891319	112096881	INTRONIC	g.112096881A>G	NC_000011.10	0.35 (G)	
UQCRB	8	rs10504961	96227901	3PRIME_UTR	g.96227901C>T	NC_000008.11	0.37 (T)	
UQCRQ	5	rs803224	132870812	UPSTREAM	g.132870812G>A	NC_000005.10	0.18 (G)	
		rs17624157	132868339	UPSTREAM	g.132868339G>A	NC_000005.10	0.05 (A)	
GDF9	5	rs39830	132865726	UPSTREAM	g.132865726G>A	NC_000005.10		
		rs30177	132866719	5PRIME_UTR	g.132866719C>G	NC_000005.10	0.36 (C)	3**,4**

SNP Name: dbSNP 149, Ensemble release 89. MAF: Minor allele frequency. HGVS name: nomclature following Human Genome Variation Society guidelines